FIG. 1

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Cancer analysis system

Proteome standard production means — 102

Proteome comparison means — 104

Disease analysis means — 106

Input/Output Interface — 108

Controlling means — 110

Input means — 112

Output means — 114

Database — 116

FIG. 2

Pre-processing means	~210	Image processing means	~212
		Feature extraction means	~214
Evolutionary classification means	~220	GA processing means	~222
		SVM application means	~224
Fuzzy rule-based classification means	~230	Data mapping means	~232
		Rule-based classification means	~234

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FIG. 3

```
                    ┌──────────────┐
                    │    Start     │
                    └──────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │       Input of proteome          │──── S101
        └──────────────────────────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │  Production of proteome standard  │──── S102
        └──────────────────────────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │    Input of proteome of a subject │──── S103
        └──────────────────────────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │  Extraction of feature data from  │──── S104
        │     proteome of the subject       │
        └──────────────────────────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │     Comparison of proteomes       │──── S105
        └──────────────────────────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │    Identification and analysis    │──── S106
        │      development of cancer        │
        └──────────────────────────────────┘
                            │
                            ▼
        ┌──────────────────────────────────┐
        │     Display of analysis results   │──── S107
        └──────────────────────────────────┘
                            │
                            ▼
                    ┌──────────────┐
                    │     End      │
                    └──────────────┘
```

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FIG. 4

```
                          ┌─────────────┐
                          │    Start    │
                          └─────────────┘
                                 │
                                 ▼
              ┌────────────────────────────────────┐
              │ Pre-processing step: image          │
              │ processing, extraction of features  │  ~ S201
              └────────────────────────────────────┘
                        ╱              ╲
                       ╱                ╲
                      ▼                  ▼
        ┌──────────────────────┐   ┌──────────────────────┐
        │  Performance of GA   │   │ Mapping of fuzzy data │
        └──────────────────────┘   └──────────────────────┘
                   │  S202                   │  S205
                   ▼                         ▼
        ┌──────────────────────┐   ┌──────────────────────────┐
        │  Application of SVM   │   │ Rule-based classification │
        └──────────────────────┘   └──────────────────────────┘
                   │  S203                   │  S206
                   ▼                         ▼
        ┌──────────────────────┐   ┌──────────────────────────┐
        │   Production of       │   │  Production of rule base  │
        │  estimation pattern   │   └──────────────────────────┘
        └──────────────────────┘            S207
                   S204
```

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FIG. 5

Serum proteome image

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FIG. 6

Population-1
(Each object has
**5-20 key features
among n features**)

ID	Spot1 density	Spot2 density	...	Cancer?

SVM → Margin of f(x)

SVM → Margin of f(x)

SVM → Margin of f(x)

SVM → Margin of f(x)

SVM → Margin of f(x)

Population-2
(next generation)

ID	Spot1 density	Spot2 density	- - -	Cancer?

Population-n

ID	Spot1 density	Spot2 density	- - -	Cancer?

Optimal key features and decision function

ID	Spot1 density	Spot2 density	...	Cancer?

Image Processing

FIG. 7

Support Vector Machine

Feature3
(spot3)

O O

O

O O

O

O O

O

Decision surface

X X X

X

X X X

X X

X X

Feature1
(spot1)

Feature2
(spot2)

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FIG. 8A

20 images of serum proteome from 30 breast cancer patients

20 images of serum proteome from 30 normal individuals

FIG. 8B

SSP	Marchset.G	Center x<n	Center y<n	Size x<mun	Size Y<mun	Peak Val	Quantity	Nom Qty	Quantity
110S	C1 Final/0	25.9899	41.0663	1.0288	0.7912	16.5442	4230.842	176.0852	97
111S	C1 Final/0	28.675	42.9189	1.0449	0.4642	20.8736	5236.707	240.7224	95
112S	C1 Final/0	28.0331	41.9257	1.1202	0.8597	31.0714	9182	388.2851	97
113S	C1 Final/0	29.3657	41.7323	1.0247	0.7455	24.1615	5798.292	422.2917	99
114S	C1 Final/0	27.6031	41.7544	0.8212	0.4522	4.7495	555.3295	41.7784	13
115S	C1 Final/0	33.2851	43.9281	1.016	0.7448	30.2488	7191.598	448.4164	97
116S	C1 Final/0	27.1828	40.6686	1.1074	0.7559	25.1038	6601.519	244.5058	99
117S	C1 Final/0	32.5738	42.1211	1.0726	0.7902	37.6688	10029.18	428.8831	98
118S	C1 Final/01	27.2045	42.2972	1.1202	0.6986	14.0222	3447.34	141.5822	98
119S	C1Fingd/01	31.8777	42.1948	1.0158	0.7457	29.5808	7019.912	285.0572	97
120S	C1Fingd/01	29.6574	41.3133	1.3979	0.821	52.6542	18983.55	843.4718	93
121S	C1Fingd/01	28.852	43.5612	1.3252	0.6421	8.0967	2164.358	153.8448	90
122S	C1Fingd/01	36.4325	40.7705	0.9115	0.0526	49.2358	12021.8	605.4489	90
123S	C1Fingd/01	28.9931	42.9507	0.9167	0.8118	68.5405	1615.3	659.6889	97
124S	C1Fingd/01	27.8638	40.8808	1.2403	0.7922	53.6314	16555.51	608.477	89
125S	C1Fingd/0	30.7217	41.0087	0.8925	0.7091	14.2607	2841.588	136.1634	74
126S	C1Fingd/0	29.2185	40.4291	1.3175	0.8509	40.7272	14344.78	549.9252	97
127S	C1Fingd/0	29.5828	42.9781	1.1112	0.7324	10.9538	2000.84	160.9054	89
128S	C1Fingd/0	27.0591	42.6235	1.0841	0.6368	16.6895	3617.098	217.9024	94
129S	C1Fingd/0	28.3744	38.7607	1.1028	0.813	61.2741	17260.21	718.549	95
130S	C1Fingd/0	31.3961	39.3158	1.2052	0.781	19.4416	5775.543	242.838	87
131S	C1Fingd/0	0	0	0	0	0	160.2212	7.0755	0
132S	C1Fingd/0	33.7845	39.9755	0.5715	1.1018	16.4832	3295.184	126.9553	67
133S	C1Fingd/0	30.1279	39.4207	0.7128	0.9507	11.7366	2408.564	103.4831	52

Spot information as a result of analysis of 2D images

FIG. 8C

```
training1.txt - 메모장
파일(F)  편집(E)  검색(S)  도움말(H)
-1    1:0.10469      2:0.697725    3:0.194961    4:0.694044    5:0.0858921
-1    1:0.607702     2:0.611268    3:0.324889    4:0.83951     5:0
-1    1:0.305028     2:0.593538    3:0.444831    4:0.196162    5:0
-1    1:0.935767     2:0.6941      3:0.599006    4:0.383446    5:0
-1    1:0.368797     2:0.937645    3:0.73533     4:0.594774    5:0.004052
-1    1:0.251766     2:0.67489     3:0.620942    4:0.32962     5:0.455162
-1    1:0.268831     2:0.672278    3:0.470859    4:0.20504     5:0
-1    1:0.323321     2:0.692317    3:0.741731    4:0.612879    5:1
-1    1:0.587885     2:0.723582    3:0.715855    4:0.268364    5:0.476582
-1    1:0.791674     2:0           3:0.7621      4:0.476857    5:0.79177
-1    1:0            2:0.768455    3:0.681397    4:0.483412    5:0
-1    1:0.508975     2:0.769142    3:0.834057    4:0.534767    5:0
-1    1:0.114086     2:0.686675    3:0.558879    4:0.858539    5:0.233969
-1    1:0.59887      2:0           3:0.467294    4:0.097549    5:0.167253
-1    1:0.119543     2:0.663873    3:0.680977    4:0.404648    5:0
 1    1:0.856679     2:0.881026    3:0.671866    4:0.486842    5:0
 1    1:0.091151     2:0.758483    3:0.451989    4:0.144411    5:0
 1    1:0.628173     2:0.668667    3:0.492968    4:0.889735    5:0
 1    1:0.129938     2:0.707562    3:0.478118    4:0.065713    5:0
 1    1:0.132144     2:0.685462    3:0.642347    4:0.22013     5:0
 1    1:0.072495     2:0.707788    3:0.496983    4:0.130244    5:0
 1    1:0.167183     2:0.68850     3:0.476744    4:0.158823    5:0.44212
 1    1:0.351353     2:0.642065    3:0.491678    4:0.269793    5:0
 1    1:0.282883     2:0.646962    3:0.474754    4:0.122441    5:0
 1    1:0.129132     2:1           3:0           4:0.555828    5:0
 1    1:0.788577     2:0.895335    3:0.234184    4:0.293345    5:0
 1    1:0.888821     2:0.693331    3:0.345997    4:0.23493     5:0.747501
 1    1:0.940586     2:0.786749    3:0.1358531   4:0.898833    5:0.58611
 1    1:0.407529     2:0.745321    3:0.241465    4:0.586292    5:0
 1    1:0.838120     2:0.628559    3:0.119552    4:0.101486    5:0.973087
```
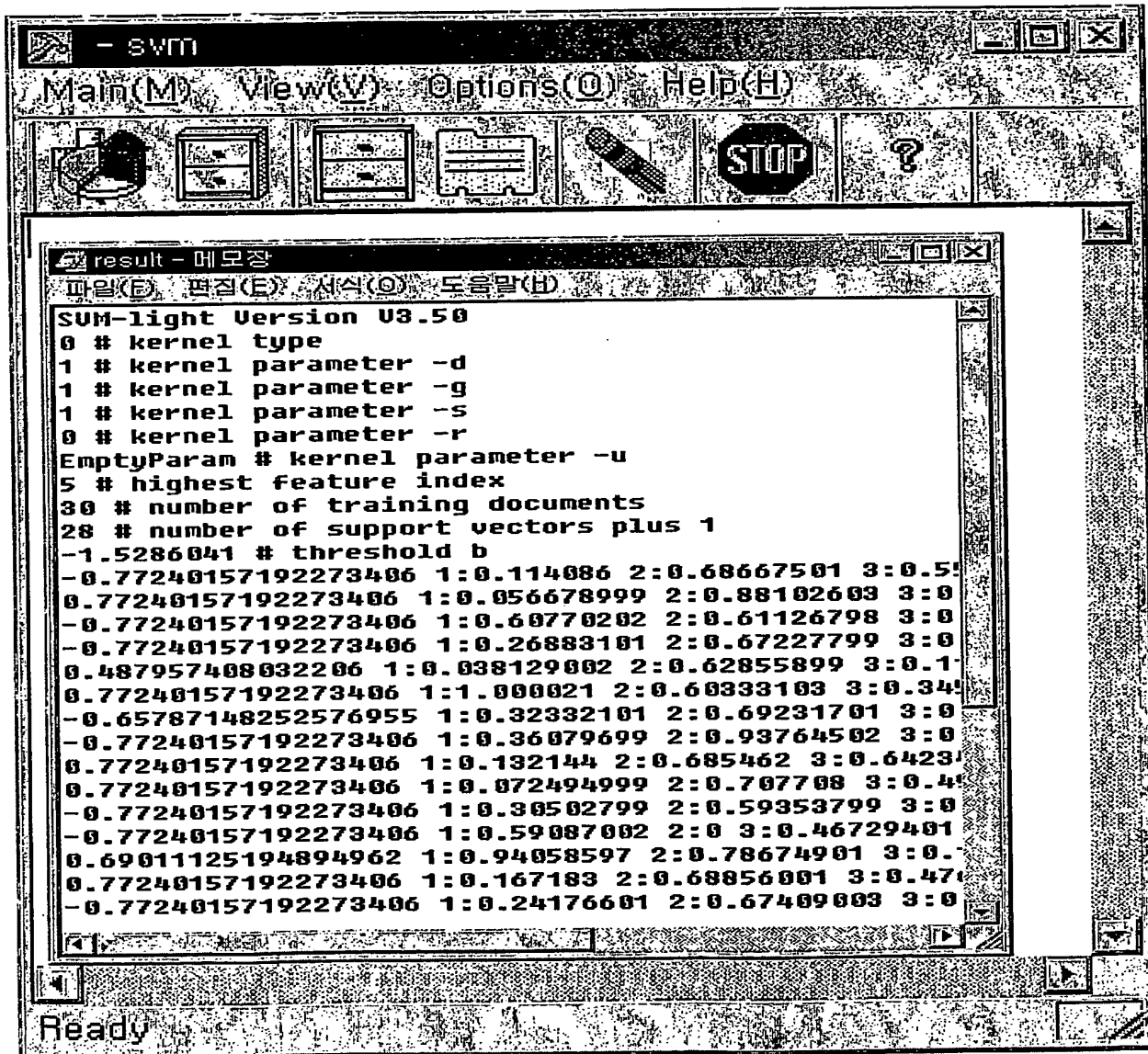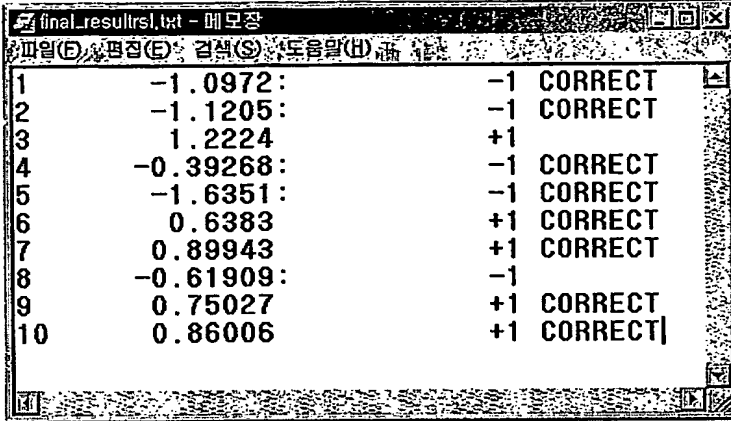
Processed training set

FIG. 8D
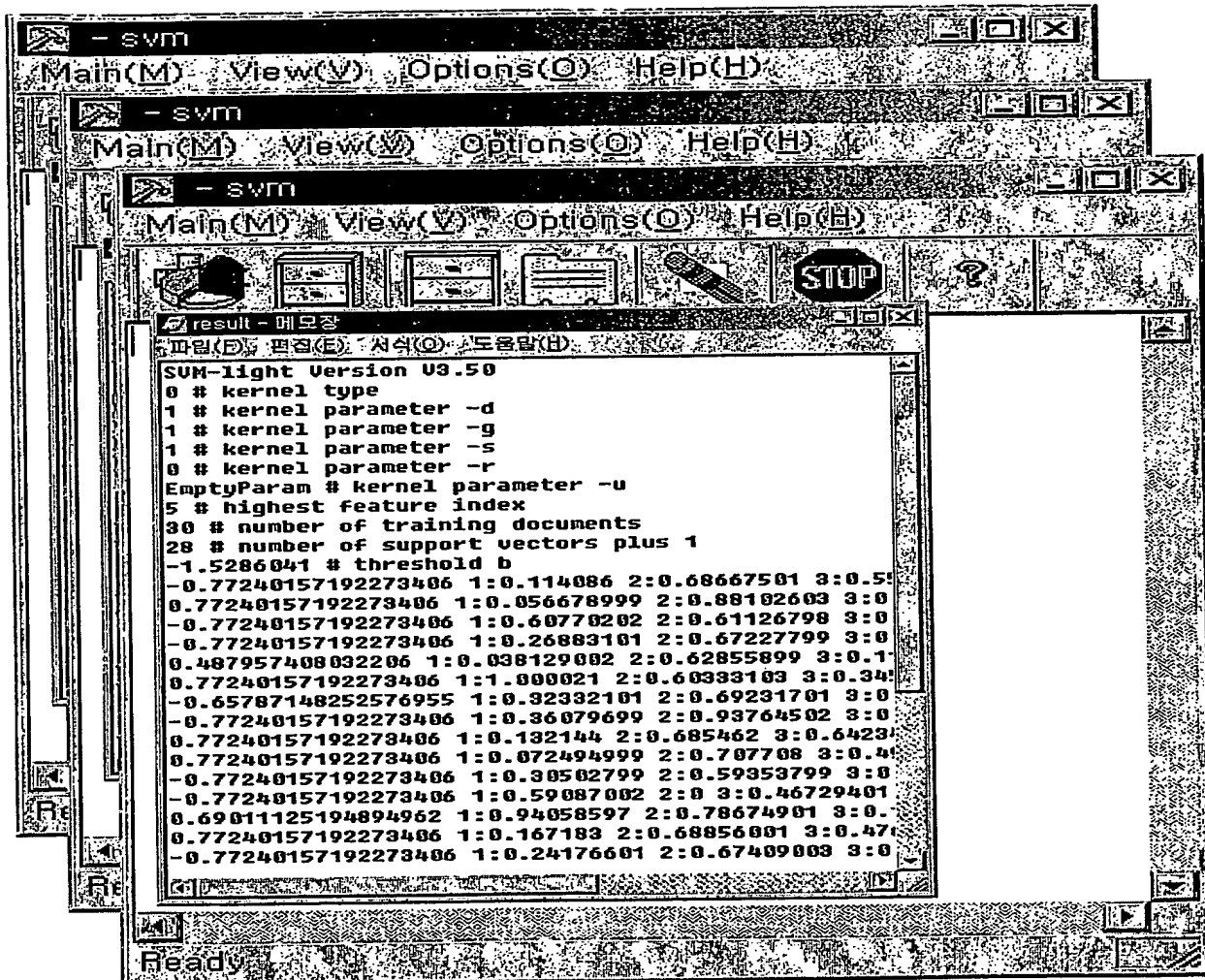
Application of SVM/GA

FIG. 9A

**Test Set of individuals
(cancer 33, normal 35)**

classify1.txt - 메모장

파일(F) 편집(E) 검색(S) 도움말(H)

−1	1:0.653996	2:0.856751	3:0.785041	4:0.080331	5:0.142553
−1	1:0.303655	2:0.69068	3:1 4:0.726181 5:0		
−1	1:0.08852	2:0.655191	3:0.234804	4:0.14616 5:0	
−1	1:0.460967	2:0.621134	3:0.824271	4:0.41638 5:0.02018	
−1	1:0.799965	2:0.660263	3:0.827914	4:1 5:0.349266	
1	1:0.123412	2:0.95635	3:0.424201	4:0.216259 5:0	
1	1:0.317662	2:0.742086	3:0.463054	4:0.092377 5:0	
1	1:0.493387	2:0.655585	3:0.828893	4:0.509369 5:0.159146	
1	1:0.151278	2:0.860072	3:0.430383	4:0.283809 5:0	
1	1:0.112535	2:0.610522	3:0.467818	4:0 5:0.344098		

FIG. 9B

```
SVM-light Version V3.50
0 # kernel type
1 # kernel parameter -d
1 # kernel parameter -g
1 # kernel parameter -s
0 # kernel parameter -r
EmptyParam # kernel parameter -u
5 # highest feature index
30 # number of training documents
28 # number of support vectors plus 1
-1.5286041 # threshold b
-0.77240157192273406 1:0.114086 2:0.68667501 3:0.5
0.77240157192273406 1:0.056678999 2:0.88102603 3:0
-0.77240157192273406 1:0.60770202 2:0.61126798 3:0
-0.77240157192273406 1:0.26883101 2:0.67227799 3:0
0.48795740803220 1:0.038129002 2:0.62855899 3:0.1
0.77240157192273406 1:1.000021 2:0.60333103 3:0.34
-0.65787148252576955 1:0.32332101 2:0.69231701 3:0
-0.77240157192273406 1:0.36079699 2:0.93764502 3:0
0.77240157192273406 1:0.132144 2:0.685462 3:0.6423
0.77240157192273406 1:0.072494999 2:0.707708 3:0.4
-0.77240157192273406 1:0.30502799 2:0.59353799 3:0
-0.77240157192273406 1:0.59087002 2:0 3:0.46729401
0.69011125194894962 1:0.94058597 2:0.78674901 3:0.
0.77240157192273406 1:0.167183 2:0.68856001 3:0.47
-0.77240157192273406 1:0.24176601 2:0.67409003 3:0
```

Decision Model

FIG. 9C


```
final_resultrsl.txt - 메모장
파일(F)  편집(E)  검색(S)  도움말(H)
1      -1.0972:      -1  CORRECT
2      -1.1205:      -1  CORRECT
3       1.2224       +1
4      -0.39268:     -1  CORRECT
5      -1.6351:      -1  CORRECT
6       0.6383       +1  CORRECT
7       0.89943      +1  CORRECT
8      -0.61909:     -1
9       0.75027      +1  CORRECT
10      0.86006      +1  CORRECT
```

Judgment results

- **Sensitivity → 100%**
- **Specificity → 88.57%**
- **Classification**
  Accuracy → 94.11%

FIG. 10

final_result_correct - 메모장

파일(F)   편집(E)   서식(O)   도움말(H)

1	Value: -0.028090	CORRECT
2	Value: -0.063031	CORRECT
3	Value: -0.070359	CORRECT
4	Value: -0.143969	CORRECT
5	Value: -0.432804	CORRECT
6	Value: -0.065068	CORRECT
7	Value: -0.254395	CORRECT
8	Value: -0.549400	CORRECT
9	Value: -0.008596	CORRECT
10	Value: -0.111672	CORRECT
11	Value: -0.297110	CORRECT
12	Value: -0.026087	CORRECT
13	Value: -0.168022	CORRECT
14	Value: -0.444805	CORRECT
15	Value: -0.070969	CORRECT
16	Value: -0.113657	CORRECT
17	Value: -0.356628	CORRECT
18	Value: -0.033568	CORRECT
19	Value: -0.103226	CORRECT
20	Value: -0.032592	CORRECT
21	Value: -0.719609	CORRECT
22	Value: -0.070134	CORRECT
23	Value: -0.076287	CORRECT
24	Value: -0.114122	CORRECT
25	Value: -0.388866	CORRECT
26	Value: -0.072279	CORRECT
27	Value: -0.063312	CORRECT
28	Value: -0.015094	CORRECT
29	Value: -0.001590	CORRECT
30	Value: -0.240725	CORRECT
31	Value: -0.551444	CORRECT
32	Value: -0.131061	CORRECT
33	Value: -0.050204	CORRECT

final_result_correct - 메모장

파일(F)   편집(E)   서식(O)   도움말(H)

34	Value: 0.128098	CORRECT
35	Value: 0.152050	CORRECT
36	Value: 0.143676	CORRECT
37	Value: 0.471308	CORRECT
38	Value: 0.023612	CORRECT
39	Value: 0.220375	CORRECT
40	Value: 0.423242	CORRECT
41	Value: 0.205883	CORRECT
42	Value: 0.026667	CORRECT
43	Value: 0.396419	CORRECT
44	Value: 0.208644	CORRECT
45	Value: 0.379373	CORRECT
46	Value: 0.130483	CORRECT
47	Value: 0.088871	CORRECT
48	Value: 0.250706	CORRECT
49	Value: 0.222808	CORRECT
50	Value: -0.008513	
51	Value: 0.540522	CORRECT
52	Value: 0.211443	CORRECT
53	Value: 0.157327	CORRECT
54	Value: 0.031818	CORRECT
55	Value: 0.036034	CORRECT
56	Value: 0.210711	CORRECT
57	Value: 0.253144	CORRECT
58	Value: 0.124807	CORRECT
59	Value: 0.305226	CORRECT
60	Value: 0.136499	CORRECT
61	Value: -0.109483	
62	Value: 0.052921	CORRECT
63	Value: 0.155490	CORRECT
64	Value: 0.356410	CORRECT
65	Value: 0.025654	CORRECT
66	Value: -0.256264	
67	Value: 0.257911	CORRECT
68	Value: -0.242207	